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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 06:00:32 ; Search time 681 Seconds  
(without alignments)  
8770.725 Million cell updates/sec

Title: US-10-617-962-2

Perfect score: 1008

Sequence: 1 atggtttatcaattacacc.....ctcattataaataatgta 1008

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
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21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1008	100.0	1008	17	US-10-617-962-2
2	663.8	65.9	1107	17	US-10-617-962-1
3	663.8	65.9	1205	17	US-10-617-962-5
4	51	5.1	8056	18	US-10-473-126-386
5	50.6	5.0	188971	17	US-10-235-192A-27
6	49.8	4.9	11394	15	US-10-240-453-95
7	48.8	4.8	1866	16	US-10-349-680-73
8	48.2	4.8	2767	17	US-10-301-533-23
9	47.6	4.7	16217	15	US-10-311-455-597
10	47.4	4.7	942	8	US-08-781-986A-531
11	47.4	4.7	942	17	US-10-329-624-531

12	47.4	4.7	158001	17	US-10-211-179-11	GENERAL INFORMATION
13	47	4.7	549	10	US-09-991-936-879	Sequence 879, App
14	47	4.7	11052	17	US-10-257-166-68	Sequence 68, App
15	46.4	4.6	260	17	US-10-424-559-100851	Sequence 100851
16	46.4	4.6	8056	18	US-10-473-126-240	Sequence 240, App
17	46.2	4.6	34722	18	US-10-322-281-700	Sequence 700, App
18	46	4.6	32392	19	US-10-706-635-27	Sequence 27, App
19	45.6	4.5	18283	17	US-10-221-613-326	Sequence 326, App
20	45.4	4.5	235070	13	US-10-087-192-1990	Sequence 1990, App
21	45.2	4.5	4985	14	US-10-094-240-10	Sequence 10, App
22	45.2	4.5	4985	16	US-10-056-405-10	Sequence 10, App
23	45.2	4.5	13377	15	US-10-311-455-1436	Sequence 1436, App
24	45.2	4.5	13377	17	US-10-221-714A-198	Sequence 198, App
25	45	4.5	6103	15	US-10-311-455-1664	Sequence 1664, App
26	44.8	4.4	1046	13	US-10-027-632-10421	Sequence 10421, App
27	44.8	4.4	1046	17	US-10-027-632-10421	Sequence 600, App
28	44.8	4.4	3399	18	US-10-793-639-600	Sequence 58879, App
29	44.6	4.4	973	17	US-10-424-539-58879	Sequence 4589, App
30	44.6	4.4	1488	9	US-09-815-242-4589	Sequence 8559, App
31	44.6	4.4	1491	9	US-09-815-242-8559	Sequence 8174, App
32	44.6	4.4	13508	17	US-10-282-132A-8174	Sequence 120, App
33	44.6	4.4	13508	17	US-10-329-624-120	Sequence 120, App
34	44.6	4.4	13508	17	US-10-312-841-1	Sequence 1, App
35	44.6	4.4	3673778	16	US-10-424-539-102915	Sequence 102915, App
36	44	4.4	609	17	US-10-706-635-69	Sequence 69, App
37	44	4.4	831	19	US-10-311-455-285	Sequence 285, App
38	44	4.4	18683	15	US-10-240-452-33	Sequence 33, App
39	44	4.4	18683	16	US-10-706-635-24	Sequence 24, App
40	44	4.4	50000	19	US-10-312-841-2	Sequence 2, App
41	44	4.4	3673778	16	US-10-741-601-5659	Sequence 5659, App
42	43.8	4.3	54775	18	US-10-741-601-5659	Sequence 17684, App
43	43.8	4.3	3673778	16	US-10-312-841-1	Sequence 1, App
44	43.8	4.3	3673778	16	US-10-311-455-286	Sequence 286, App
45	43.6	4.3	6418	15	US-10-311-455-286	Sequence 296, App

#### ALIGNMENTS

RESULT 1  
US-10-617-962-2  
; Sequence 2, App  
; Publication No. US20040055036A1  
GENERAL INFORMATION:  
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation  
; APPLICANT: EAST, Peter David  
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photobacterium  
; FILE REFERENCE: 050179-0076  
; CURRENT APPLICATION NUMBER: US/10/617,962  
; CURRENT FILING DATE: 2003-07-14  
; PRIOR APPLICATION NUMBER: US/09/463,048A  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: PCT/AU98/00562  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: PO 8088  
; PRIOR FILING DATE: 1997-07-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1008  
; TYPE: DNA  
; ORGANISM: Photobacterium luminescens  
US-10-617-962-2

Query Match 100.0%; Score 1008; DB 17; Length 1008;  
Best Local Similarity 100.0%; Pred. No. 1.9e-198;  
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTATCAATTAAACACCTGATGATGAAGTGAATATCCACCGTTGAAACAAATA 60  
Db 1 ATGTTATCAATTAAACACCTGATGATGAAGTGAATATCCACCGTTGAAACAAATA 60





Best Local Similarity 45.3%; Pred. No. 2.6;  
Matches 226; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

[illegible]

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RESULT 5
US-10-235-192A-27
: Sequence 27, Application US/10235192A
: Publication No. US20040043389A1
: GENERAL INFORMATION:
: APPLICANT: McCarthy, Jeanette
: TITLE OF INVENTION: Methods and Compositions for Identifying
: TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases
: TITLE OF INVENTION: and Disorders Associated Therewith
: FILE REFERENCE: WMT-011
: CURRENT APPLICATION NUMBER: US/10/235.192A
: CURRENT FILING DATE: 2002-09-04
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 27
: LENGTH: 188971
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 145329-145428, 187896-187995, 195894-195993
: OTHER INFORMATION: N = any nucleotide
US-10-235-192A-27

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Query Match	5.0%;	Score 50.6;	DB 17;	Length 188971;
Best Local Similarity	42.6%;	Pred. No. 10;		
Matches 263;	Conservative 0;	Mismatches 354;	Indels 0;	Gaps 0;

[illegible]

Db	103669	ATGAATATCTATATGCAATATCTATATATGCAATATCTATGAAATATCTATATATGCAATATCT	103748
QY	132	ATATGACCTTAAGAAAATATATATTAAGCTTACGCTTGGCTGTAAGTGTAATCATATGCT	191
Db	103749	ATTATGAATATACATGAATATATATGAAATATATATGAAATATATATGAAATATCTATATGAAATATAT	103808
QY	192	ATCTAAATCTTCTGATGACTATATATAGAAATPAAAGACCTGCTGAGAGAAATTTATCAAA	251
Db	103809	ATGAATATCTATGAAATATCTATATGAAATATATATGAAATATCTATATGAAATATATATATG	103868
QY	252	ATATATGCTATCTTTCATCTGACACTATTAAGTGAAATAGTGATCAATTTCTAAGA	311
Db	103869	AATATATATGAAATTTATATATGAAATATATATATGAAATATATATATGAAATTTATATATGA	103928
QY	312	TATGGCAATAGCTTTTATTAAGATGAACGTGATTTGAGGTCATATCTCAAAACAT	371
Db	103929	TATATATATGAAATATATATATGAAATATATGAAATATATATATATATATATATATGAAAT	103988
QY	372	TTGGAATCTTCTGACCTGAAAATPAAACATGAGTGCTTATTCAGATGACGATPAAAT	431
Db	103989	TATATATGAAATATATATATGAAATATATATATGAAATATATATATATATATATATATGAAATAT	104048
QY	432	ATTAGCACTATATTTTTCTCTGTACAGAAATTCACCTGAGAGAAATCAACATCAAA	491
Db	104049	TATATGAAATATATATATGAAATATATATATGAAATATATATATATATATATATATATATAT	104108
QY	492	TGCCGCAAGATTTTAAATTAATGATTTCTTATTTACCTATCTGCTGTAACCTCACT	551
Db	104109	TGAATTAATATATGAAATATATATATGAAATATATATATATATATATATATATATATATATGCA	104168
QY	552	GCGAAGAGAGATTTTTTCAAAAACTTTTACAGATGATTAAGGCTTAATCATTAGAGAA	611
Db	104169	ATTATATATGAAATATATATATATGAAATATATATATATATATATATATATATATATATATGAAAT	104228
QY	612	TTATATTTGAGAGAAAA 628	
Db	104229	ATATATGAAATATATATAT 104245	

```

RESULT 6
US-10-240-453-95
/ Sequence 95, Application US/10240453
/ Publication No. US20030148326A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
/ TITLE OF INVENTION: Transcription
/ TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
/ FILE REFERENCE: 5013.1009
/ CURRENT APPLICATION NUMBER: US/10/240,453
/ PRIOR FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: PCT/EP01/03973
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 350
/ SEQ ID NO 95
/ LENGTH: 11394
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-95

```

Query Match	4.9%	Score 49.8;	DB 15;	Length 11394;
Best Local Similarity	50.6%;	Pred. No. 5.3;		
Matches 120;	Conservative	0;	Mismatches 117;	Indels 0;
			Gaps	.0

OY	124	GGAATTGAAATTCAGACTGAGAAATAATATTAGCTTACGCTTGGCTGTAAGTGTAT	183
Db	318	GGAAATGCAATTAGAGTGGTAAAGATTTTGAATGAATTTAGTTTAAGTTATATATAT	377
OY	184	CATAATGTATCTTAACTTCTCGTAGCACTATTATTAAGAAATTAAGAGCTGCTGAGAAATT	243
Db	378	ATATATTATATATTAATTAATATGTATATATATATATAATTAATTAATATGTATATT	437
OY	244	TATCAAGAAATATATCTTAATCTTTCATCTGCACTTTTAGGTGAATAATGCTATCAAAATT	303
Db	438	AAGGTTTAGTATTATTTATATATATTATTTATTTGTTTGTAGTTAGAGAAAGGTTTAAAGAAATTA	497
OY	304	TCTAAGATATGCGCAAAATGGTTTTTATATAAGATGAACCTGATTTTGAAGCTCAATAT	360
Db	498	TGATATTTTATTAGTAATGATGTGATTTTAGTCTTTTAGAGCTTTTTCGTTTTTAATAT	554

```

RESULT 7
US-10-349-680-73
: Sequence 73, Application US/10349680
: Publication NO. US20030176654A1
: GENERAL INFORMATION:
: APPLICANT: Cassell, Gall
: APPLICANT: Chen, Bilsen
: APPLICANT: Glaes, Jennifer
: APPLICANT: Glaes, John
: APPLICANT: Heiner, Cheryl
: APPLICANT: Lefkowitz, Elliot
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
: TITLE OF INVENTION: UREAlyticUM
: FILE REFERENCE: UAB-13403/22
: CURRENT APPLICATION NUMBER: US/10/349,680
: CURRENT FILING DATE: 2003-01-23
: PRIOR APPLICATION NUMBER: US 09/601,198
: PRIOR FILING DATE: 2000-12-08
: PRIOR APPLICATION NUMBER: PCT/US99/01972
: PRIOR FILING DATE: 1999-01-29
: PRIOR APPLICATION NUMBER: US 60/073,189
: PRIOR FILING DATE: 1998-01-30
: NUMBER OF SEQ ID NOS: 181
: SOFTWARE: Patentin version 3.2
: SEQ ID NO 73
: LENGTH: 1866
: TYPE: DNA
: ORGANISM: Ureaplasma urealyticum
US-10-349-680-73

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Query Match	4.8%;	Score 48.8;	DB 16;	Length 1866;
Best Local Similarity	47.3%;	Pred. No. 4.4;		
Matches 249;	Conservative	0;	Mismatches 267;	Indels 10;
				Gaps 3

Qy	122	ATGCAATTGAATATAGACTAAGAAAATATATATAGCTACCGTTGCTGTAAAGGTGA	181
Db	1037	ATGAAAAAAAAACAAGAAATTAAGATATATTTAGATCTTTTGATTAAGATTAAGATTAAT	1099
Qy	182	TTCATATATGTATCTAAACCTTCCGTAGACTATATATPAAGATTAAGAGACTGTGAGAGA-	240
Db	1097	TTCAAAAAATATATATATCATATATTAAGATATTAATTAATTAATTAATTAAGAGAGCAT	115
Qy	241	--ATTATCAAGATATATATGTCTAATCTTCACTGCACTATAGGTGAATGTGATC	298
Db	1157	ATATTACACAAAAATTAATTAATAATCTTTATATAGATGCTTCAATATATTAATGATGTTTC	121
Qy	239	AAATTTCTAAAGATATGCGAAATGAGTTTATATPAAGATGACGTGATTTTGAAGGTCAAT	358
Db	1217	AAATTACAAAATATCTAATATCAACAACAAATGATPAAGAAATACAAATATTAATTAATTAAC	127
Qy	359	ATCTCTAAAACATTTTGAATGTCTTCTGAGCTTGAAAAATTAACCAATGAGTCTTATTCAG	418

Db	1277	AATTAATAGATTAGTAATATTAATTTTAAAAACCAAAAAACCAAGAGATTCTAATGAAT	1336
Qy	419	ATGACGATTAAT-----ATTAGCATATATTTTTCTGTGCAGGAAATTCACGTGA	473
Db	1337	ATTAAGCAAAATTTAAATGATTATGCAAAAAATTTTTCACAAATTTGTAATTTTATTTAA	1396
Qy	474	GGAAATCAACATCAAAATGCCGACAGTTTAAAAATTAATGATTTCTTAATTACCTT	533
Db	1397	TGAATTTTAAAGCA--CTTTAATTTAAATTTTAAATTAATGATTTTACCTTACCAAAACAAT	1454
Qy	534	ATCTGCTGAATCTCACTGGGAAGAGATTTTTTCAAAAAACCTTTTNCATGATTTAGA	593
Db	1455	AAATCCATATTACATAAGATGTTAGGACCAAGGAAAAATATTTAAAAAGGTAAAAAA	1514
Qy	594	GGCTTAATCATTTGAGAAATATATTTAGAGAAAAAACTTTCTTAA	639
Db	1515	ACTTAAACCATGAGAGATTATTTTTCATTAATATTAATTTTAGAA	1560

```

RESULT 8
US-10-301-533-23
; Sequence 23, Application US/10301533
; Publication No. US20030203473A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Microbial Sumo Protease Homologs
; FILE REFERENCE: P-IJ 5488
; CURRENT APPLICATION NUMBER: US/10/301,533
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 60/331,895
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2767
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1507)
US-10-301-533-23

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Query Match	4.8%;	Score 48.2;	DB 17;	Length 2767;
Best Local Similarity	56.7%;	Pred. No. 6.7;		
Matches	89;	Conservative	0;	Mismatches 68;
			Indels	0;
			Gaps	0;

Oy	243	TTATCAAGAAATATATGTCTATCTTTGATCTGCACATTTAGGGAATAATGGTATCAAT	302
Db	562	TGATCTGATRAAAAATTTCTCTGTTTCTAAATTCATTTCAGTAAAAAATATGACAAAAT	621
Oy	303	TTCTAAAGATATGGCAATGGTTTTTAATAAGATGAATCGAATTTTGAGGTCATATCC	362
Db	622	GTGTAATGAAGATGATGAGATCATTTTTTAAATATAATAAAATATATTTTAAAGATAATGATGC	681
Oy	363	TCAAAACATTTGGAATGTTCTCGATCTTGAAAAATAAA	399
Db	682	TGATGAAGTATCAATATATATAGATGATGACTATAAA	718

```

RESULT 9
US-10-311-455-597
; Sequence 597. Application US/10311455
; Publication No. US20030143606a1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of diseases
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455

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/ CURRENT FILING DATE: 2002-12-16  
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537  
/ PRIOR FILING DATE: 2001-07-02  
/ PRIOR APPLICATION NUMBER: DE 10032529.7  
/ PRIOR FILING DATE: 2000-06-30  
/ PRIOR APPLICATION NUMBER: DE 10043826.1  
/ PRIOR FILING DATE: 2000-09-01  
/ NUMBER OF SEQ ID NOS: 2424  
/ SEQ ID NO 597  
/ LENGTH: 16217  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
/ FEATURE:  
/ NAME/KEY: unsure  
/ LOCATION: 12269  
/ OTHER INFORMATION: n is a o r g o r c o r t  
/ US-10-311-455-597

Query Match 4.7%; Score 47.6; DB 15; Length 16217;  
Best Local Similarity 43.3%; Pred. No. 17; Mismatches 289; Indels 0; Gaps 0;  
Matches 221; Conservative 0;

QY 124 GGAATTGAATTCGAGCTAAGAAATATATATAGCTTACGCTTGGCTGAAGTGTATT 183  
DB 2495 GAAATATATGTAATTTTATTAATAAATTAAGAAATGTAATATATAAGATGTAATG 2554  
QY 184 CATTAATGTAATCTAAACTTCTGATGACTTATTAAGATTAAGAGACTGCTGAGAAATT 243  
DB 2555 AAGAAATAATTAATAATTAATTAATTTTATTAATAAATTAAGTTTGTATATTA 2614  
QY 244 TATCAAGATATATGCTATCTATCTGATCGACTATGGAATAAGTGATCAAAATT 303  
DB 2615 TGGGGTTGTTATGTTATATATTTTATTAATTAATTAAGAAATGTAATTA 2674  
QY 304 TCTAAGATATGCAATGCTTTTATTAAGATGAATGCTGAAATGCTCAATATCCT 363  
DB 2675 TATATTAATTAATTAATTAATTTTATTAATGTTAATAATTAATTAATTAATTA 2734  
QY 364 CAAACATTTGGAGTCTCCGAGCTTGAAATTAACATGAGTCTTATTCAGATGAC 423  
DB 2735 AAGGTATTAATTAATTTGCTTATGTAATTTTATTAATTAATTAATTAATTAAT 2794  
QY 424 GATTAATTTAGCACTATATTTTCTGTAACAGAAATCCATGAGGAAATCA 483  
DB 2795 AGTATTTAGTTAGATTTTATTAATTTTATTAATTAATTAATTAATTAATTAAT 2854  
QY 484 CAATCAATGCGCAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 2854  
DB 2855 TTTTAAATTAATTAAGAAATTTGTTTGTGCTTATGTTTATGTTGAAAGGATTT 2914  
QY 544 ACTTCACTGGAGAGAGATTTTTCAAAAAATTTTAACATGATTAAGAGCTAAATCA 603  
DB 2915 AGTATGAGTTTATTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 2974  
QY 604 TTAGAGATTTATTTAGAGAAAAAACTT 633  
DB 2975 AGTGGAAATTTTATTAAGAAATTAATTAATTT 3004

## RESULT 10

US-08-781-986A-531  
/ Sequence 531, Application US/08781986A  
/ Publication No. US20030054436A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Charles Kunsch  
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
/ NUMBER OF SEQUENCES: 5255  
/ CORRESPONDENCE ADDRESSES:  
/ ADDRESSEE: Human Genome Sciences, Inc.  
/ STREET: 9410 Key West Avenue  
/ CITY: Rockville

/ STATE: Maryland  
/ COUNTRY: USA  
/ ZIP: 20850  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
/ COMPUTER: HP Vectra 486/33  
/ OPERATING SYSTEM: MSDOS version 6.2  
/ SOFTWARE: ASCII Text  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/781,986A  
/ FILING DATE:  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER:  
/ FILING DATE:  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Benson, Bob  
/ REGISTRATION NUMBER: 30,446  
/ REFERENCE/DOCKET NUMBER: PB248BP  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (301) 309-8504  
/ TELEFAX: (301) 309-8512  
/ INFORMATION FOR SEQ ID NO: 531:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 942 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ US-08-781-986A-531

Query Match 4.7%; Score 47.4; DB 8; Length 942;  
Best Local Similarity 47.8%; Pred. No. 6; Mismatches 151; Indels 0; Gaps 0;  
Matches 138; Conservative 0;

QY 66 AGATATGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 125  
DB 313 AAAAAAGTACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 372  
QY 126 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 185  
DB 373 AGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 432  
QY 186 TAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 245  
DB 433 CATTAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 492  
QY 246 TCAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 305  
DB 493 AACGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 552  
QY 306 TAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 354  
DB 553 AAAACAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 601

## RESULT 11

US-10-329-624-531  
/ Sequence 531, Application US/10329624  
/ Publication No. US20040043037A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Charles Kunsch  
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
/ NUMBER OF SEQUENCES: 5256  
/ CORRESPONDENCE ADDRESSES:  
/ ADDRESSEE: Human Genome Sciences, Inc.  
/ STREET: 9410 Key West Avenue  
/ CITY: Rockville  
/ STATE: Maryland

	Matches	410;	Conservative	0;	Mismatches	536;	Indels	11;	Gaps	3;
Qy	57	AATGCGAGGAGTATTAGTGCTATATCTAACTTTAAGCAACAGATGAGGGTCATTCACG	116							
Db	126950	AAT	127009							
Qy	117	ATCATATGGAATTTGAATTT-----CGAGCTAAGAAAATAATATAGCTTAAGCTTGGCTG	172							
Db	127010	ATAATTAAT	127068							
Qy	173	TNAGGTGATTCATTAATGTATCTAAACTTCCTGATGACTATATATTAAGAATTAAGACATG	232							
Db	127070	TAAAAATTAATA	127129							
Qy	233	CTGAGAGATTTATCAGAGATATATATGCTAATCTTTCAITCTGCACATTAGGTGAAAAATG	292							
Db	127130	TATATTAATA	127189							
Qy	293	GTGATCAAATTTCTAAAGATATGCGAAATGGTTTTATATAAGATGAACGTGATTTTGAAG	352							
Db	127190	ATATATTAAT	127249							
Qy	353	GTCAATATCCCTCAAAACAATTTGGAATGTCTCGAGCTTGAAATATAACCATGAGTGCCTT	412							
Db	127250	ATTAATA	127309							
Qy	413	ATTGAGATGAGATTAATTAATTTAGCACATATATTTTCTCTG-----TACAGAAATTC	466							
Db	127310	TTATATATTAATA	127369							
Qy	467	CACGTGAGAGAAATTCACATCCAATGCCGCAAGTTTTTAAATTAATGATTTCTTAT	526							
Db	127370	TA	127429							
Qy	527	TTACCTTATCTGCTGTAACCTTCACGTGGAGAGAGATTTTTTCAAAAACTTTTACAATG	586							
Db	127430	ATA	127488							
Qy	587	GATTAGAGGCTTAATCATTAGAGATTAATTTAGAGAAAAAAACCTTCTAACCCTTCT	646							
Db	127490	TATATATA-TAT	127548							
Qy	647	TTGCAACACCGCAGAGATTACCTGATGCGAGATATGGTATTGGCTGCAACACGAAG	706							
Db	127549	AT	127608							
Qy	707	CGCCTTAATGAGAGTGGATTTAAGAACTTAAATAACAAATCTAGAGATGATTTT	766							
Db	127609	ATAAT	127668							
Qy	767	CTAATATGGAAGGGGCTGCAAAACMAAGTATAGTTCATTTTATTAAGAAGGTACAAAGG	826							
Db	127669	ATA	127728							
Qy	827	GTAACGCTCCACAGACAGACAGCAAGAAAGTATTTGTACAGCCAGTGGCACTAACCCTGAAA	886							
Db	127729	TAAATA	127788							
Qy	887	AATTGCCGAATTAATTTATATATAGTGTGAGAGCTTAAGCCAAAGAACAGAGGTAACTTTACTC	946							
Db	127789	ATA	127848							
Qy	947	AAATATGATCTGACAATATCAATGACGTTCACTAGTGTGAACCTCATTTAAAAATA	1003							
Db	127849	ATA	127905							

RESULT 13  
 US-09-991-936-879/c  
 ; Sequence 879, Application us/09991936  
 ; Publication No. US20030073827A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brandt, Kevin S.



APPLICANT: Gaines, Patrick J.  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF  
FILE REFERENCE: PC-6-CI  
CURRENT APPLICATION NUMBER: US/09/991,936  
CURRENT FILING DATE: 2001-11-21  
PRIOR APPLICATION NUMBER: US/09/543,668  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/128,704  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 1959  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 879  
LENGTH: 549  
TYPE: DNA  
ORGANISM: Ctenocephalides felis  
US-09-991-936-879

Query Match 4.7%; Score 47; DB 10; Length 549;  
Best Local Similarity 49.0%; Pred. No. 6.6; Mismatches 130; Indels 0; Gaps 0;  
Matches 125; Conservative 0;

QY 372 TTGGAATGTTCCGAGCTTGAATAATTAACCATTTGAGTCTTATTCAGATGAGATAAATT 431  
DB 335 TTTTATATAGCTTAAGTTACTTTAAATAATATGCTTTTGTCAATATGAGATATGGA 276  
QY 432 ATTGACATATATTTTCTCTGTACAGAAATTCACCTGAGAGAAATCAATCAAA 491  
DB 275 TGTAAAGACACATTTCTTTTTCATATGCAAAATTTGACATCAATCATTTTAAAGCTTCATT 216  
QY 492 TGCCGGAAGATTTTAAATTAATGATTTCTTATTTACTATCTGCTGTAACCTCACT 551  
DB 215 TTCCATACCATTTATAGATATGATGCAATATGGAACCTTACTTTTCAATGAGTTT 156  
QY 552 GGAAGAGAGATTTTTCAAAAAATTTTACATGATGATGAGGCTTAATCAATGAGAA 611  
DB 155 TAGACATATATATTTTAACTTAATGTTGACTTCAATTAAGAGGAAATTAATTTTATA 96  
QY 612 TTATATTTGAGAAA 626  
DB 95 TCAGTGTATGAAA 81

RESULT 14  
US-10-257-166-68  
Sequence 68, Application US/10257166  
Publication No. US20040023230A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIERENBERG, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of  
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics  
FILE REFERENCE: 5013.1011  
CURRENT APPLICATION NUMBER: US/10/257,166  
CURRENT FILING DATE: 2002-10-07  
PRIOR APPLICATION NUMBER: PCT/EP01/07470  
DE 10032529.7  
DE 10043826.1  
PRIOR FILING DATE: 2001-06-29  
2000-06-30  
2000-09-01  
NUMBER OF SEQ ID NOS: 178  
SEQ ID NO 68  
LENGTH: 11052  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-257-166-68

Query Match 4.7%; Score 47; DB 17; Length 11052;  
Best Local Similarity 48.7%; Pred. No. 20; Mismatches 128; Conservative 0; Indels 0; Gaps 0;

QY 225 AGAGCTGCTGAGAGAAATTTATCAAGATATATGCTTAATCTTATCTGACCTATTGG 284  
DB 1196 AGAAAGTATGATGATATTTTAAAGTTTGGGTTTTTTTGAAGATATATATATGG 1255  
QY 285 TGAATAATGATCAATTTTCTAAAGATATGCAATGTTTATTAAGAAATGAATGCA 344  
DB 1256 AGTAAATGTTTAAATAAGTGAAGAAAGTGAAGAAAGGGGTTTATTTATTTGAGATTAAGTT 1315  
QY 345 TTTTGAAGTCAATATCTCAAAACATTTGGAATGTTCTGAGCTTGAATAATCAAT 404  
DB 1316 TTTATAGTATTTTATTAATAAGGGGTTTGGGTGAAGTATGATTAATAATAAGTTT 1375  
QY 405 GAGTCTTATTCAGATGAGATTAATTTTACACTATATTTTCTCTGTACAGAAAT 464  
DB 1376 AAAAATTAATAATTAATTTGATATTTTATGTTATTTTGTATTTATATAGATTA 1435  
QY 465 TCCACTGAGAGAAATCAACAAAT 487  
DB 1436 TTGAGCTTTTGAATAATTTATAGT 1458

RESULT 15  
US-10-424-599-100851  
Sequence 100851, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 100851  
LENGTH: 260  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_62081C.1  
US-10-424-599-100851

Query Match 4.6%; Score 46.4; DB 17; Length 260;  
Best Local Similarity 52.6%; Pred. No. 6.6; Mismatches 101; Conservative 0; Indels 91; Indels 0; Gaps 0;

QY 249 AGAATATATGCTTAATCTTCACTGACATATTAAGTGAATAATGATCAATTTCTAA 308  
DB 1 ATTAACGTATATACCTTTTAAACATTTTATGCAAAAAGGACTGAAGTTTCGA 60  
QY 309 AGATATGCAATATGTTTATTAAGAATGAACTGATTTTGAAGTCAATATCCCAAAA 368  
DB 61 AAAAAGAGAAATATGATTTTCAAGTTCTTCTACCTGAAATATTTTAAACATCAAC 120  
QY 369 CATTTGAGATGTTCTGAGCTTGAATAATTAACATTTGAGTCTTATTCAGATGAGATTA 428  
DB 121 CGTTTGATTTTAAAAAATGACATTAACAAAGTTTGTCTATCTTAAGGGGGGAAA 180  
QY 429 ATTATTAAGCACT 440  
DB 181 AAACCTTACTACT 192

Search completed: March 1, 2005, 08:28:53  
Job time : 696 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 02:15:26 ; Search time 211 Seconds  
(without alignments)  
7816.905 Million cell updates/sec

Title: US-10-617-962-2

Perfect score: 1008

Sequence: 1 atggttatacaattacacc.....cccatataaataatata 1008

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents NA:  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/PCUTS\_COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1008	100.0	1008	4 US-09-463-048A-2	Sequence 2, Appl1
2	663.8	65.9	1107	4 US-09-463-048A-1	Sequence 1, Appl1
3	663.8	65.9	1205	4 US-09-463-048A-5	Sequence 5, Appl1
4	628.2	62.3	1272	2 US-08-569-168-6	Sequence 6, Appl1
5	521.4	51.7	834	2 US-08-569-168-3	Sequence 3, Appl1
6	521.4	51.7	837	2 US-08-569-168-1	Sequence 1, Appl1
7	62.6	6.2	1141	4 US-09-806-708B-22	Sequence 22, Appl1
8	59.8	5.9	7218	1 US-08-232-463-14	Sequence 14, Appl1
9	51	5.1	1055	4 US-09-806-708B-23	Sequence 23, Appl1
10	50.6	5.0	1141	4 US-09-806-708B-22	Sequence 22, Appl1
11	48.8	4.8	1866	4 US-09-601-198-153	Sequence 153, App
12	47.8	4.7	729	3 US-09-134-001C-1161	Sequence 1161, App
13	47.6	4.7	1055	4 US-09-806-708B-23	Sequence 23, Appl1
14	47.4	4.7	942	4 US-08-956-171E-531	Sequence 531, App
15	47.4	4.7	942	4 US-08-781-986A-531	Sequence 531, App
16	47.4	4.7	41708	3 US-09-470-512A-3	Sequence 3, Appl1
17	47.4	4.7	41708	4 US-09-676-519-18	Sequence 18, Appl1
18	47.4	4.7	5340	4 US-09-627-122-21	Sequence 21, Appl1
19	46.6	4.6	95255	4 US-09-949-016-17067	Sequence 17067, A
20	44.8	4.4	3399	4 US-09-614-221A-600	Sequence 600, App
21	44.8	4.4	451924	4 US-09-949-016-12896	Sequence 12896, A
22	44.8	4.4	451925	4 US-09-949-016-12896	Sequence 12896, A
23	44.6	4.4	13508	4 US-08-956-171E-120	Sequence 120, App
24	44.6	4.4	13508	4 US-08-781-986A-120	Sequence 120, App
25	44.4	4.4	44653	4 US-09-949-016-11944	Sequence 11944, A
26	44.4	4.4	44653	4 US-09-949-016-15690	Sequence 15690, A
27	44	4.4	832	4 US-09-621-976-2813	Sequence 2813, App

C	28	43.8	4.3	665	2 US-08-883-795A-36	Sequence 36, Appl1
C	29	43.2	4.3	1470	4 US-09-830-217-1	Sequence 1, Appl1
C	30	43.2	4.3	1470	4 US-10-278-946-1	Sequence 1, Appl1
C	31	42.8	4.2	7425	3 US-09-453-702B-212	Sequence 212, App
C	32	42.6	4.2	5340	4 US-09-627-122-21	Sequence 21, Appl1
C	33	42.6	4.2	640681	4 US-09-790-988-1	Sequence 1, Appl1
C	34	42.4	4.2	627	4 US-09-248-796A-14060	Sequence 14060, A
C	35	42.4	4.2	22896	4 US-09-949-016-17127	Sequence 17127, A
C	36	42.2	4.2	5136	4 US-08-956-171E-332	Sequence 332, App
C	37	42.2	4.2	5136	4 US-08-781-986A-332	Sequence 332, App
C	38	41.8	4.1	2557	4 US-09-710-279-3829	Sequence 3829, App
C	39	41.8	4.1	3146	4 US-09-710-279-4281	Sequence 4281, App
C	40	41.8	4.1	3646	4 US-09-710-279-4070	Sequence 4070, App
C	41	41.4	4.1	978	4 US-09-248-796A-5337	Sequence 5337, App
C	42	41.4	4.1	1318	4 US-09-925-637-1	Sequence 1, Appl1
C	43	41.4	4.1	2424	4 US-08-956-171E-392	Sequence 392, App
C	44	41.4	4.1	2424	4 US-08-781-986A-392	Sequence 392, App
C	45	41.2	4.1	2142	4 US-09-107-532A-905	Sequence 905, App

#### ALIGNMENTS

RESULT 1	US-09-463-048A-2
Sequence 2, Application US/09463048A	
Patent No. 6630619	
GENERAL INFORMATION:	
APPLICANT: Commonwealth Scientific and Industrial Research Organisation	
APPLICANT: EAST, Peter David	
TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photo.	
TITLE OF INVENTION: luminescens	
FILE REFERENCE: 050179-0076	
CURRENT APPLICATION NUMBER: US/09/463, 048A	
PRIOR FILING DATE: 2002-12-13	
PRIOR APPLICATION NUMBER: PCT/AU98/00562	
PRIOR FILING DATE: 1998-07-17	
PRIOR APPLICATION NUMBER: PO 8088	
PRIOR FILING DATE: 1997-07-17	
NUMBER OF SEQ ID NOS: 20	
SOFTWARE: Patentin version 3.1	
SEQ ID NO 2	
LENGTH: 1008	
TYPE: DNA	
ORGANISM: Photorhabdus luminescens	
US-09-463-048A-2	
Query Match	100.0%; Score 1008; DB 4; Length 1008;
Best Local Similarity	100.0%; Pred No. 6.7e-244;
Matches 1008; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGTATACATTAACACCTGATGATAGAGTATCCACCGTTGAAAGCAATTA 60
DB	1 ATGGTATACATTAACACCTGATGATAGAGTATCCACCGTTGAAAGCAATTA 60
QY	61 GCGAGATATAGTACTGATTAACCTTAAGCAACAGATGAGGTATACAGATCA 120
DB	61 GCGAGATATAGTACTGATTAACCTTAAGCAACAGATGAGGTATACAGATCA 120
QY	121 TATGGAATGATATGACCTAAGAAATTAATTAAGCTTGGCTGAATGGT 180
DB	121 TATGGAATGATATGACCTAAGAAATTAATTAAGCTTGGCTGAATGGT 180
QY	181 ATTGATATGATATCTTAACCTTCCTGATGATTAATTAAGATTAAGAGCTGAGAG 240
DB	181 ATTGATATGATATCTTAACCTTCCTGATGATTAATTAAGATTAAGAGCTGAGAG 240
QY	241 ATTATCAAGATATATGCTTAATCTTATGCTGCACTTTGAGTAAATGATGCA 300
DB	241 ATTATCAAGATATATGCTTAATCTTATGCTGCACTTTGAGTAAATGATGCA 300
QY	301 ATTTCGAAGATATGCAATGCTTTTATTAAGATGAATGATTTGAAGGCAATAT 360
DB	301 ATTTCGAAGATATGCAATGCTTTTATTAAGATGAATGATTTGAAGGCAATAT 360

Db 301 ATTCTAAAGATATGCGAAATGCTTTTATATAGATGAACCTGATTTTGAAGCTCAATAT 360  
Qy 361 CCTCAAAACATTTGGATGTTCTCGAGCTGAAATATAACATATGAGTCTTATTCAGAT 420  
Db 361 CCTCAAAACATTTGGATGTTCTCGAGCTGAAATATAACATATGAGTCTTATTCAGAT 420  
Qy 421 GACGATTAATTTATGACATATATTTTCTCTGTCAGGAAATTCATCTGAGGAAAT 480  
Db 421 GACGATTAATTTATGACATATATTTTCTCTGTCAGGAAATTCATCTGAGGAAAT 480  
Qy 481 CAACATCAAAATGCGCAAGATTTTAAATTAATTAATTTCTATTTACCTATTCGCT 540  
Db 481 CAACATCAAAATGCGCAAGATTTTAAATTAATTAATTTCTATTTACCTATTCGCT 540  
Qy 541 GTAACCTCACTGGAGAGAGATTTTTCATAAAACCTTTTACATGGAATTAAGAGCTAAA 600  
Db 541 GTAACCTCACTGGAGAGAGATTTTTCATAAAACCTTTTACATGGAATTAAGAGCTAAA 600  
Qy 601 TCATTAAGAGATTAATTTGAGAGAAAAAACTTTCTTAAACCTTTCTTTCGACCGCAG 660  
Db 601 TCATTAAGAGATTAATTTGAGAGAAAAAACTTTCTTAAACCTTTCTTTCGACCGCAG 660  
Qy 661 AGATTAACCTGAGAGAGATTAATTTGCTGAGCAACAGAGAGCGCTTAAATGAGAGA 720  
Db 661 AGATTAACCTGAGAGAGATTAATTTGCTGAGCAACAGAGAGCGCTTAAATGAGAGA 720  
Qy 721 GTGAGTTTAAAGACCTTAAATACAAATCTAGAGATGATTTTCTAATATGAGAGG 780  
Db 721 GTGAGTTTAAAGACCTTAAATACAAATCTAGAGATGATTTTCTAATATGAGAGG 780  
Qy 781 GCTGCAAAACAAAGATATGTTTATTAATAAGAGATCAAAAGGATACGCTCCACAG 840  
Db 781 GCTGCAAAACAAAGATATGTTTATTAATAAGAGATCAAAAGGATACGCTCCACAG 840  
Qy 841 ACAGCAGCAAAAGATTTGCTACAGCAGAGAGATACCTGSAATTAATTCGGAATAT 900  
Db 841 ACAGCAGCAAAAGATTTGCTACAGCAGAGAGATACCTGSAATTAATTCGGAATAT 900  
Qy 901 TTATATAGTGTGAGGCTAAGCCAAAGACAGGGTAACTTTTACTCAAAATGATATCTGAC 960  
Db 901 TTATATAGTGTGAGGCTAAGCCAAAGACAGGGTAACTTTTACTCAAAATGATATCTGAC 960  
Qy 961 AATACATGACGGTCAATGTTGGAACCTATTAATAATATATGA 1008  
Db 961 AATACATGACGGTCAATGTTGGAACCTATTAATAATATATGA 1008

RESULT 2  
US-09-463-048A-1  
; Sequence 1, Application US/09463048A  
; Patent No. 6630619  
; GENERAL INFORMATION:  
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation  
; APPLICANT: EAST, Peter David  
; TITLE OF INVENTION: Toxin Genes from the Bacteria *Xenorhabdus nematophilus* and *Photobacterium*  
; FILE REFERENCE: 050179-0076  
; CURRENT APPLICATION NUMBER: US/09/463,048A  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: PCT/AU98/00562  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR FILING DATE: 1997-07-17  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1107  
; TYPE: DNA  
; ORGANISM: *Xenorhabdus nematophilus*  
US-09-463-048A-1

Query Match 65.9%; Score 663.8; DB 4; Length 1107;  
Best Local Similarity 79.4%; Pired. No. 2.6e-157;

Matches 835; Conservative 0; Mismatches 162; Indels 54; Gaps 2;  
Qy 12 ATTAACACCTGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 71  
Db 57 AGTAAACGCTGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 116  
Qy 72 AGTAAACGCTGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 131  
Db 117 AATAGGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 176  
Qy 132 AATAGGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 191  
Db 177 AATAGGATGATAGATGATATATCCACCCGTTGAAAGCAATAGCAGAGATAT 236  
Qy 192 ATCTAAACCTTCGATGATGATATATAGATGATATAGATGATGATGATGATGATGAT 251  
Db 237 CTCTAAACCTTCGATGATGATATATAGATGATATAGATGATGATGATGATGATGAT 296  
Qy 252 ATATATGCTTAATCTTCACTGATGATGATATAGATGATGATGATGATGATGATGAT 311  
Db 297 ATATATGCTTAATCTTCACTGATGATGATATAGATGATGATGATGATGATGATGAT 356  
Qy 312 TATGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371  
Db 357 TATGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416  
Qy 372 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431  
Db 417 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476  
Qy 432 ATTAGCACTATATATTTTCTCTGATGATGATGATGATGATGATGATGATGATGAT 491  
Db 477 ATTAGCACTATATATTTTCTCTGATGATGATGATGATGATGATGATGATGATGAT 536  
Qy 492 TCCCGCAATTTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 551  
Db 537 TCCCGCAATTTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 596  
Qy 552 GGAAGAGAGATTTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 611  
Db 597 GGAAGAGAGATTTTAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 656  
Qy 612 TTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671  
Db 657 TTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 716  
Qy 672 TGGCAGATAGATTTTGGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 714  
Db 717 TGGCAGATAGATTTTGGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 776  
Qy 715 -----TGGAGAGAGATTTTAAAGACTTAA 740  
Db 777 TACAGCAACAGCTTACAGAGCTTCAATCTAATTTGAGAGATTTTGCAGAGAGCTTAA 836  
Qy 741 AATATCAAAATCTAGAGATGATTTTCTAATATGAGAGAGAGAGAGAGAGAGAGAT 800  
Db 837 AGATTAACCATCAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 896  
Qy 801 TTATATTAATAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 860  
Db 897 TTATATTAATAAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 956  
Qy 861 TACAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917  
Db 957 TACAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1016  
Qy 918 AAGCAAAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 977  
Db 1017 AAGCAAAAGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076  
Qy 978 TAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008  
Db 1077 TAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107

Db 673 TTATATTGAGAGAAAAAATTCTTAACCTTTCTTTCGACCAACCGAGAGTTACCTGA 73

Matches 833: Conservative 0:

Query Match	62.3%;	Score 638.2;	DB 2;	Length 1272;
Best Local Similarly	79.1%;	Pred. No. 2:se-14;		
Matches 833, Conservative	0;	Mismatches 163;	Indels 57;	Gaps 5;





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; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZapC-F18
;
US-08-232-463-14
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Matches 25; Conservative 225; Mismatches 167; Indels 0; Gaps 0;

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RESULT 9
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; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using SW model

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(without alignments)  
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Listing first 45 summaries

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DB 841 ACAGAGAGCAAAAGATTTGTGACAGCAGGTGCAAGTAACTGGAATAATGCGAATAT 900
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DB 961 AATAAATGACGGTTCATAGTGTGGAATCTCATTTAAATAATATATGA 1008

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## RESULT 2

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; Sequence 1, Application US/10617962
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin genes from the Bacteria Xenorhabdus nematophilus and Photob
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
US-10-617-962-1

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Query Match 65.9%; Score 663.8; DB 58; Length 1107;
Best Local Similarity 79.4%; Pred. No. 1.4e-135;
Matches 835; Conservative 0; Mismatches 162; Indels 54; Gaps 2;

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DB 57 AATAACCTGATGAGAGATAGTTATTTGGCTGAGCCAAAGAGAGCGCTTAATGAGAGA 116
QY 72 AGTACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 131
DB 117 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 176
QY 132 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 191
DB 177 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 236
QY 192 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 251
DB 237 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 296
QY 252 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 311
DB 297 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 356

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DB 597 GGAAGAGAGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 656
QY 612 TTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 671
DB 657 TTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 716
QY 672 TGAGAGATGAGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 714
DB 717 TGAGAGATGAGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 776
QY 715 TGAGAGATGAGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 740
DB 777 TGAGAGATGAGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 836
QY 741 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 800
DB 837 AATACGATATCTTAACCTTAAGCAACAGATGAGGCTCATACGATCATATGAGATGA 896
QY 801 TTGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 860
DB 897 TTGATTTTAAAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 956
QY 861 TACAGCAGATGAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 917
DB 957 TACAGCAGATGAGATGAGATGTTTGAAGTCAATATCTCAAAACAT 1016
QY 918 AAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 977
DB 1017 AAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1076
QY 978 TAGTGTGAGATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1008
DB 1077 TAGTGTGAGATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1107

```

## RESULT 3

```

US-10-617-962-5
; Sequence 5, Application US/10617962
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin genes from the Bacteria Xenorhabdus nematophilus and Photob
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1

```





QY 641 CTCTTTTCGACCGCAGAGATTAAGTATGAGTATTTGGTCGACCA 700  
DB 1364 RRR 1305  
QY 701 CAGACGCTTAATGAGAGTATTTAAGAACTTAATAAATACTAGAAATG 760  
DB 1304 RRR 1245  
QY 761 GATTTCTAATGAGAGGCTGCAAAACAAAGTATGATTTATTAAGAGTAC 820  
DB 1244 RRR 1185  
QY 821 AAAAGGTAAGCTCCAGACAGACGCAAAAGTATTTGTAAGCAGAGTAAAC 880  
DB 1184 RRR 1125  
QY 881 TGGAAATTTGCGCAATTAATTTATAGTGAAGCTAAGCAAAAGAGGTTAA 937  
DB 1124 RRR 1068

RESULT 5  
PCT-US99-26796-234  
; Sequence 234, Application PC/TUS9926796  
; GENERAL INFORMATION:  
; APPLICANT: United States Government as Represented by the  
; APPLICANT: Secretary of the Navy  
; TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite  
; TITLE OF INVENTION: Plasmodium falciparum and Proteins of Said  
; TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and  
; TITLE OF INVENTION: Diagnostic Reagents  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: PCT/US99/26796  
; CURRENT FILING DATE: 1999-11-05  
; NUMBER OF SEQ ID NOS: 420  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 234  
; LENGTH: 3927  
; TYPE: DNA  
; ORGANISM: Plasmodium falciparum  
PCT-US99-26796-234

Query Match 5.2%; Score 52.6; DB 1; Length 3927;  
Best Local Similarity 43.9%; Pred. No. 0.87;  
Matches 212; Conservative 0; Mismatches 344; Indels 3; Gaps 1;

QY 24 TGATGAAGTATGATTCACCGCTGAAAGAAATGAGAGATATAGTACT 83  
DB 2511 TATATTTGTAATATTCATTTGAATAATAATTAATTCATATGATGATGATATAT 2570  
QY 84 AAACCTTAAGCAAGATGAGGTCATACAGATCATATGAAATGAGATGACCTAA 143  
DB 2571 AACACATGATTTTAAATAGTACTTATGAAAATATTAAGTTGATTAATATGAG 2630  
QY 144 GAAAAATATATGCTTACCTTGGCTGATGATGATGATGATGATGATGATGATG 203  
DB 2631 TGAATATATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 2690  
QY 204 TGATGATATATATA---AGAAATAAGAGCTGCTGAGAGAAATTAACAAGATATATGTC 260  
DB 2691 TAAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2750  
QY 261 TAACTCTTCACTGACATATTAAGTGAATAATGATGATGATGATGATGATGATG 320  
DB 2751 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2810  
QY 321 TGGTTTTTAAGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATG 380  
DB 2811 TGGTGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2870  
QY 381 TCCTGAGCTTGAATATTAACATGATGATGATGATGATGATGATGATGATGATGATG 440  
DB 2871 TGTGAAAAATTTATGAAAGACAAATAAGCTTTAATGAAGTGAAGAAATGAGACA 2930

QY 441 ATATTTTTCTGTACAGAAATTCACGAGAGAAATCAACATCAATGCGCAG 500  
DB 2931 AGATATAAAGAAATATAGCAAAAAGAGATATGATTTATGATTTATGATGATG 2990  
QY 501 ATTTTAAATTAATGATTTCTTATTTATCTTATCTGCTGATTAATCTTCACTGAGAG 560  
DB 2991 TATGATATATGATTTATGATTAAGAAAGGGAATGATGATTAATGATTAATGAG 3050  
QY 561 GATTTTCAAAAACCTTTAATGATGATTAAGAGCTAATATCATTAAGATTAATGAT 620  
DB 3051 ATATTCAGAAAATATATGATGATTAATATGATTAAGCAATGAACTGTTATGAGTGC 3110  
QY 621 GAGAAAAAACCTTTCAAA 639  
DB 3111 TATGTTAAAAATGATAAA 3129

RESULT 6  
US-10-990-328-94720/C  
; Sequence 94720, Application US/10990328  
; GENERAL INFORMATION:  
; APPLICANT: CARILL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL001495  
; CURRENT APPLICATION NUMBER: US/10/990,328  
; CURRENT FILING DATE: 2004-11-17  
; NUMBER OF SEQ ID NOS: 558824  
; SOFTWARE: PatSeq for Windows Version 4.0  
; SEQ ID NO 94720  
; LENGTH: 709368  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(709368)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-990-328-94720

Query Match 5.2%; Score 52; DB 67; Length 709368;  
Best Local Similarity 45.7%; Pred. No. 4.9; Length 709368;  
Matches 169; Conservative 3; Mismatches 198; Indels 0; Gaps 0;

QY 449 TCTCTGACAGAAATTCACGAGAGAAATCAACATCAATGCGCAGATTTT 508  
DB 674585 TATCTATCAACAATCAAAAATTAAGAAATGATGATGATGATGATGATGATG 674526  
QY 509 AATTAATGATTTCTTATTTACCTTATCTGCTGTAACCTTCACTGAGAGATTTT 568  
DB 674525 TAAACATTAATATTCATTTTATGATGATTAATAAATACATCAATGATGATG 674466  
QY 569 CAAAAAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATG 628  
DB 674465 TGAATATTTATCTGTTTATTTACTGTAAGTTACAGAAAGTATTAATGATG 674406  
QY 629 AACTTCTAAACCTTTCTTTCACACCGCAGAGATTAACGATGAGAGATTTT 688  
DB 674405 TCTTTATTTGCTGCTCTTAAATATTTTGTATTTCTCCCTCAATATGATG 674346  
QY 689 TGGCTGACCAAGAGAGGCTTAATGAGAGTGTATTAAGAACTTAATAATTAAC 748  
DB 674345 GATGAAATCGAGAAATTAAGCTGAATTTATCTATCTCAATTTATTAATAAGATTA 674286  
QY 749 AATCTAAGATGATTTCTTAATGATGAGAGGCTGCAAAACAAAGTATGATTTA 808  
DB 674285 ATTTAAGATGATTTTAAAGATGTTTGAATATTAATCACTCCAGTGTGAGCTTGA 674226  
QY 809 TAAAGAGT 818  
DB 674225 ATTAAGAGT 674216





```
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
/ TITLE OF INVENTION: Transcription
/ TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
/ FILE REFERENCE: 5013.1009
/ CURRENT APPLICATION NUMBER: US/10/240,453
/ CURRENT FILING DATE: 2002-10-02
/ PRIOR APPLICATION NUMBER: PCT/EP01/03973
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 350
/ SEQ ID NO 95
/ LENGTH: 11394
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-95
```

```
Query Match      4.9%; Score 49.8; DB 50; Length 11394;
Best Local Similarity 50.6%; Pred. No. 4.8;
Matches 120; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 124 GGAATGATATGACCTAAGAAATATATAGCTACCTTGGCTGTAAGTGTATT 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 GGAATGATATGAGTGTAAAGATATTAAGATTAATTAAGTTAGTTTATAGATATATAT 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 CATATGATATCTTAACCTCCGATGACTATTATTAAGAAATTAAGACCTGCTGAGAAATT 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 TATCAAGATATATATGCTTAATCTTTCATCTGACATTAAGTGAATAATGCTGATCAAAATT 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 AAGGTTAGTATTTATTTATTTATTTATTTGTTTGTAGTTGAGAAGTTTGAATAATA 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 TCTAAGATATGCAAAATGTTTATTAAGAAATGACATGATTTTGAAGTCAATAT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 498 TGATATTTTATTAAGTATGATTTAGTTTGAAGTTTGTGTTTATATATAT 554
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 12  
US-09-948-124-61

```
/ Sequence 61, Application US/09948124
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig
/ TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
/ TITLE OF INVENTION: Y. METHODS OF DETECTION, AND USES THEREOF
/ FILE REFERENCE: CL001301
/ CURRENT APPLICATION NUMBER: US/09/948,124
/ CURRENT FILING DATE: 2002-12-23
/ NUMBER OF SEQ ID NOS: 183
/ SEQ ID NO 61
/ LENGTH: 318007
/ TYPE: DNA
/ ORGANISM: HUMAN
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) - (318007)
/ OTHER INFORMATION: n = A,T,C or G
US-09-948-124-61
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Query Match 4.9%; Score 49.8; DB 41; Length 318007;

Best Local Similarity 46.6%; Pred. No. 12;  
Matches 159; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

```
QY 108 TCATCAGCATCATATGGAATGATATCGACTAAGAAATATATATAGCTTACGCTTT 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133261 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 133320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 168 GCGCTGAAGTGTATTCATTAATGATCTAACTCCGATGACATATTAAGAAATAAAGA 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133321 AATTATATATATATATATATATATATATATATATATATATATATATATATATATAT 133380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 228 GACTGCTGAGAGAAATTTATCAAGATATATGCTATCTTTCATCTGCACTTTAGGCGA 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133381 TATTTAATATATATATATATATATATATATATATATATATATATATATATATAT 133440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 288 AATGCTGATCAAAATTTCTAAAGATATGCAAAATGTTTTTATTAAGAAATGATGATTT 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133441 TATTTATTAAGAAATATATATATATATATATATATATATATATATATATATATAT 133500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 348 TGAAGGTCAATATCTCAAAACATTTGGAATGCTTGAGCTTGAATAATTAACCATTTGAG 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133501 TATTAAGTAAATATCTATATATATATATATATATATATATATATATATATATATAT 133560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 408 TGCTTATTCAGATGACATTAATTTATGACATATATTTT 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 133561 TGATATTAATTAATATATATATATATATATATATATATATATATATATATATAT 133601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 13

US-09-947-911-2

```
/ Sequence 2, Application US/09947911
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig
/ TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
/ TITLE OF INVENTION: X. METHODS OF DETECTION, AND USES THEREOF
/ FILE REFERENCE: CL001300
/ CURRENT APPLICATION NUMBER: US/09/947,911
/ CURRENT FILING DATE: 2001-09-07
/ NUMBER OF SEQ ID NOS: 368
/ SEQ ID NO 2
/ LENGTH: 600322
/ TYPE: DNA
/ ORGANISM: HUMAN
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1) - (600322)
/ OTHER INFORMATION: n = A,T,C or G
US-09-947-911-2
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Query Match 4.9%; Score 49.8; DB 41; Length 600322;  
Best Local Similarity 46.6%; Pred. No. 14;  
Matches 159; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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QY 108 TCATCAGCATCATATGGAATGATATCGACTAAGAAATATATATAGCTTACGCTTT 167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 499869 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 499928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 168 GCGCTGAAGTGTATTCATTAATGATCTAACTCCGATGACATTTTAAAGAAATAAAGA 227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 499929 AATTATATATATATATATATATATATATATATATATATATATATATATATATAT 499988
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 228 GACTGCTGAGAGAAATTTATCAAGATATATGCTATCTTTCATCTGCACTTTAGGCGA 287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 499989 TATTTAATATATATATATATATATATATATATATATATATATATATATATATAT 500048
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 288 AATGCTGATCAAAATTTCTAAAGATATGCAAAATGTTTTTATTAAGAAATGATGATTT 347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500049 TATTTATTAAGAAATATATATATATATATATATATATATATATATATATATATAT 500108
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 348 TGAAGGTCAATATCTCAAAACATTTGGAATGCTTGAGCTTGAATAATTAACCATTTGAG 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500109 TATTAAGTAAATATCTATATATATATATATATATATATATATATATATATATATAT 500168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```





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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 05:41:20 ; Search time 271 Seconds  
(without alignments)  
2484.740 Million cell updates/sec

Title: US-10-617-962-2  
Perfect score: 1008  
Sequence: 1 atgcttatacaattacacc.....ctcattataaaatataatga 1008

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5184529 seqs, 334010122 residues

Total number of hits satisfying chosen parameters: 10369058

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents NA New:\*  
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9: /cgn2\_6/prodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	5.1	1134	US-10-932-182A-166160	Sequence 166160, App1
2	46	4.6	1941	US-10-691-672A-4	Sequence 4, App1
3	45.2	4.5	3089	US-10-954-778-160	Sequence 160, App
4	43.4	4.3	3089	US-10-954-778-160	Sequence 160, App
5	40.6	4.0	8093	US-10-517-441-307	Sequence 307, App
6	40.4	4.0	12610	US-10-517-441-441	Sequence 441, App
7	40.4	4.0	12610	US-10-517-441-715	Sequence 715, App
8	40.2	4.0	820	US-10-932-182A-166164	Sequence 166164, App1
9	40	4.0	1691140	US-11-021-837-43	Sequence 43, App1
10	39.8	3.9	37627	US-10-932-182A-76518	Sequence 76518, App
11	39.6	3.9	2460	US-10-517-441-414	Sequence 414, App
12	39.2	3.9	19634	US-10-517-441-414	Sequence 414, App
13	39.2	3.9	19634	US-10-517-441-688	Sequence 688, App
14	39.2	3.9	19634	US-11-044-879-3	Sequence 3, App1
15	39	3.9	1083	US-10-450-763-12549	Sequence 12549, App
16	39	3.9	2412	US-10-932-182A-6042	Sequence 6042, App
17	39	3.9	5286	US-10-517-441-293	Sequence 293, App
18	39	3.9	5286	US-10-517-441-293	Sequence 293, App
19	39	3.9	8093	US-10-517-441-581	Sequence 581, App
20	38.8	3.8	5286	US-10-517-441-294	Sequence 294, App
21	38.8	3.8	5286	US-10-517-441-568	Sequence 568, App
22	38.6	3.8	19634	US-10-517-441-414	Sequence 414, App
23	38.6	3.8	19634	US-10-517-441-414	Sequence 414, App
24	38.4	3.8	10865	US-10-517-441-463	Sequence 463, App

25	38.4	3.8	10865	US-10-517-441-737	Sequence 737, App
26	38.2	3.8	7110	US-10-517-441-322	Sequence 322, App
27	38.2	3.8	7110	US-10-517-441-596	Sequence 596, App
28	38.2	3.8	100596	PCT-US04-42189-92	Sequence 92, App1
29	38	3.8	76829	US-10-517-441-27	Sequence 27, App1
30	38	3.8	109669	US-11-021-837-41	Sequence 41, App1
31	38	3.8	363361	US-10-517-441-53	Sequence 53, App1
32	37.8	3.8	10865	US-10-517-441-464	Sequence 464, App
33	37.8	3.8	10865	US-10-517-441-738	Sequence 738, App
34	37.8	3.8	92221	US-10-014-101B-37	Sequence 37, App1
35	37.6	3.7	5286	US-10-517-441-294	Sequence 294, App
36	37.6	3.7	5286	US-10-517-441-568	Sequence 568, App
37	37.6	3.7	12610	US-10-517-441-442	Sequence 442, App
38	37.4	3.7	2743	US-11-051-267-1	Sequence 1, App1
39	37.4	3.7	8391	US-10-932-182A-166179	Sequence 166179, App
40	37.2	3.7	5286	US-10-517-441-293	Sequence 293, App
41	37.2	3.7	5286	US-10-517-441-567	Sequence 567, App
42	37.2	3.7	6327	US-10-932-182A-75787	Sequence 75787, App
43	37	3.7	4469	US-10-472-963-1492	Sequence 1492, App
44	37	3.7	10412	US-10-287-436A-56	Sequence 56, App1
45	37	3.7	10412	US-10-287-436A-317	Sequence 317, App

ALIGNMENTS

RESULT 1  
US-10-932-182A-166160  
; Sequence 166160, Application US/10932182A  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIRO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 166160  
; LENGTH: 1134  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-166160

Query Match 5.1%; Score 51; DB 6; Length 1134;  
Best Local Similarity 48.2%; Pred. No. 0.008;

Matches 144; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY	148	ATTAATTTAGCTTACCGCTTGGCTGTAAGTATTCATATGATCTTAACCTTCCGAT	207
DB	610	ATTAATTTAGCTTATTTATATTAATTAATTAATTAATTTAGTAAATATTTGTTAAAT	669
QY	208	GACTATTATTAAGATTAAGAGAGCTGCTGAGAAATTTATCAAGATATATGCTAACTT	267
DB	670	GATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	729
QY	268	TGATTCGACTATTTGCTGTAAGTATTCATATTTCAAGATATGCAATGCTTTT	327
DB	730	ATTAATTTAGCTTATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	789
QY	328	TATTAAGATTAAGCTGATTTTGAAGTCAATTCCTCAAACTTTGGAATGTTCTCGAG	387
DB	790	ATTAATTTAGCTTATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	849
QY	388	CTTGAATTAAGCTGATTTTGAAGTCAATTCCTCAAACTTTGGAATGTTCTCGAG	446
DB	850	TATTAATTAAGCTTATTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	908

RESULT 2



US-10-691-672A-4/c  
; Sequence 4, Application US/10691672A  
; GENERAL INFORMATION:  
; APPLICANT: DRIULHE, PIERRE  
; TITLE OF INVENTION: GLI3P-MSPI FUSION PROTEIN, IMMUNOGENIC COMPOSITIONS AND  
; TITLE OF INVENTION: MALARIAL VACCINES CONTAINING IT  
; FILE REFERENCE: 02356.0085  
; CURRENT APPLICATION NUMBER: US/10/691,672A  
; CURRENT FILING DATE: 2003-10-24  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 4  
; LENGTH: 1941  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-691-672A-4

Query Match 4.6%; Score 46; DB 6; Length 1941;  
Best Local Similarity 45.8%; Pred. No. 0.12;  
Matches 195; Conservative 0; Mismatches 230; Indels 1; Gaps 1;

QY 105 GGGTCATACAGCATCATATGGAATGATATCGAGCTTAAGAAATATATATAGCTTACGC 164  
DB 764 GGATCATTTGGTATGATGATTAATTTTCATGAACAAAGTTCATTTCTATTTTTCATCT 705  
QY 165 TTGGGTGATAGGTATCATATGATATCTTAACTTCTGATGACTATATATATATAT 224  
DB 704 TTAAATGTTCAATGATATATTAAGTTCAAACTTCTGATATACATTTGCAAGACCA 645  
QY 225 AGAGCTGCTGAGAGAAATTTATCAAGATATATGCTAACTTCTCATCTGACTATTAAG 284  
DB 644 TTTTCATGAAATACGTTTTTTCTTCATATATGATGTCTACCTTTTATATGCTTTCTG 585  
QY 285 TGAATATGATGATCAATATTTCTAAGATATGCAAAATGTTTTATATATATATATAT 344  
DB 584 -GGAAATGGTCTGATCTTCTTCATTTTATTAATTTTTTTCTTAATATCTTTATGTAT 526  
QY 345 TTTTGAAGTCAATATCTTCAAAACATTTGGAATGTTCTGAGCTTGAATATTAACATT 404  
DB 525 TTGTGATGAGAAAGGTTCTTAAGGTTCAATTTAATCTGTGTGATGCTTTATGTTT 466  
QY 405 GAGTGTATATGATGATGATATATATATATATATATATATATATATATATATATAT 464  
DB 465 TTGATATGAGAAAGTCTTCTGATATATATATATATATATATATATATATATATAT 406  
QY 465 TCCACTGAGAGAAATCAATCAATCAATGCGCAGATTTTAAATATATATATATAT 524  
DB 405 TTCAAGTATATCTTAATCTGATATATATATATATATATATATATATATATATAT 346  
QY 525 ATTTAC 530  
DB 345 ATTTTC 340

RESULT 3  
US-10-954-778-160/c  
; Sequence 160, Application US/10954778  
; GENERAL INFORMATION:  
; APPLICANT: ZWIEBEL, LAURENCE J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE  
; TITLE OF INVENTION: ODOURANT RECEPTORS OF SENSORY NEURONS  
; FILE REFERENCE: N1125  
; CURRENT APPLICATION NUMBER: US/10/954,778  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: 10/056,405  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/264,649  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 160  
; LENGTH: 3089  
; TYPE: DNA  
; ORGANISM: Anopheles gambiae  
US-10-954-778-160

Query Match 4.5%; Score 45.2; DB 6; Length 3089;  
Best Local Similarity 44.3%; Pred. No. 0.2;  
Matches 185; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

QY 48 TAAAAGCAATATGAGAGATATATGATATATATATATATATATATATATATATATAT 107  
DB 2217 TAAAT 2158  
QY 108 TCATACAGCATCATATGGAATGATATATGAGCTTAAGAAATATATATATATATATAT 167  
DB 2157 TAT 2098  
QY 168 GCGTGAAGTGTATTCATATATGATCTAACTTCTGATGACTATATATATATATAT 227  
DB 2097 TAAAT 2038  
QY 228 GACTCTGAGAGAAATTTATCAAGATATATGCTTAATCTTTCATCTGACATTTAGTGA 287  
DB 2037 TTAAT 1978  
QY 288 AAATGATCAATTTCTCAAAAGATATGCAAAATGTTTTTATAGAAATGAGCTGATTT 347  
DB 1977 TAAAT 1918  
QY 348 TGAAGTCAATATCTCAAAACATTTGGAATGTTCTGAGCTTGAATATTAACATTGAG 407  
DB 1917 TAAAT 1858  
QY 408 TCTTATTCAGATGAGATATATTTTATGACTATATTTTCTCTGACAGAAATTT 465  
DB 1857 TATTTGTTCTGTAAGTAAATGTTGTAATATATATATATATATATATATATATAT 1800

RESULT 4  
US-10-954-778-160  
; Sequence 160, Application US/10954778  
; GENERAL INFORMATION:  
; APPLICANT: ZWIEBEL, LAURENCE J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING CHEMICAL AGENTS WHICH STIMULATE  
; TITLE OF INVENTION: ODOURANT RECEPTORS OF SENSORY NEURONS  
; FILE REFERENCE: N1125  
; CURRENT APPLICATION NUMBER: US/10/954,778  
; CURRENT FILING DATE: 2004-09-30  
; PRIOR APPLICATION NUMBER: 10/056,405  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: 60/264,649  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 248  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 160  
; LENGTH: 3089  
; TYPE: DNA  
; ORGANISM: Anopheles gambiae  
US-10-954-778-160

Query Match 4.3%; Score 43.4; DB 6; Length 3089;  
Best Local Similarity 43.7%; Pred. No. 0.52;  
Matches 191; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 79 ATACTAACTTTAAGCAAAAGATGAGGTATATACAGCATCATATGAAATGATATGCA 138  
DB 1814 ATAAACATTTTATATACCAATTTATATACAGCAACAAATATACGAATTTATATAT 1873  
QY 139 GCTAAGAAAT 198  
DB 1874 TAT 1933

[illegible]

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RESULT 5
US-10-517-441-307
Sequence 307, Application US/10517441
GENERAL INFORMATION:
APPLICANT: FÖRKEN, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMMICH, Inko
APPLICANT: RUJAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARY, Almut
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010861
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955. 0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096. 8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779. 4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 307
LENGTH: 8093
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-307

Query Match      4.0%;   Score 40.6;   DB 7;   Length 8093;
Best Local Similarity 43.7%;   Pred. No. 2.7;   229;   Indels 0;   Gaps 0;
Matches 178;   Conservative 0;   Mismatches

QY      212  ATTATTAAGATTAAAGAGACTGCTGAGAGAAATTATCAAGATATATGCTTAATCTTCAT 271
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1467  ATTGATATAATATTGGAGAGGATTTATGAAATTAATATGGGTTTGTTTATATATAGTTT 1526

QY      272  CTGCACATTTTAGGAGAAAATGATGATCAATTTCTTAAAGATATAGCAAAATGGTTTATATA 331

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Db	1527	ATATAAGATTTTAAATTTGTTTTTTTAAAGGAAATAGAGTTGGAAATTAATTTGTTTT	1586
Qy	332	AGAAATGACTGAGATTTTGAAGTCATATCTCMAAACATTGGAAATGTTCCGAGCTTG	391
Db	1587	GGTATAAAGTAGATTTATTTAGTAGAAATATAGAAATATTTGTATTTTGTAATTAAGATG	1646
Qy	392	AAATAAACAATGAGTGCCTTATTCAGATACGATCAATTAATTAAGCACTATATTTTCT	451
Db	1647	TTTTTAATATTTTAAATTTTGTGTGTTATTTTATATATAGAAATGTGACGATAGTTTAAA	1706
Qy	452	CTGACAGAAATTCACCTGAGAGAAATCAACATCAATTAATGCGCAAGATTTTAAAT	511
Db	1707	TTTTAGATATAATTTATTTTAAATTAATAAATTTGATATGTATTTTAAATA	1766
Qy	512	TAATGATTTCTATTTAACTTATCTGCTAACTTCACTGGAGAGAGATTTTTCAA	571
Db	1767	AAGGTATTTTAAAGTAGAGATTTTAAATATAAGTAGTAATATTTACGTAGTAAGAT	1826
Qy	572	AAACCTTACATGATTAGAGGCTAAATCATTAGAGATTAATTT	618
Db	1827	AAAAAGTTAAATATTTTATATTTTAAATTTTGAAGTAAATTTT	1873

```

RESULT 6
US-10-517-441-441
; Sequence 441, Application US/10517441
GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MATER, Sabine
APPLICANT: MARTENS, John
APPLICANT: MODEL, Fabian
APPLICANT: NIMWICH, Inko
APPLICANT: RUYAN, Tamas
APPLICANT: SCHMITT, Armin
APPLICANT: SCHEITZ, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MARX, Almut
APPLICANT: HOFFER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cancer
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 441
LENGTH: 12610
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-441

Query Match      4.0%; Score 40.4; DB 7; Length 12610;
Best Local Similarity 45.9%; Pred. No. 3.2;
Matches 178; Conservative 0; Mismatches 206; Indels 4; Gaps 1;

OY      231 TGCTGAGAGAATTATCAAGAAATATATGTCTAATCTTTCACTGCACATAAGTGAAAA 290
Db       7753 TGGTGTAGATTAAGAAAGATATATGTAAATTAATTAAGAAAGATTTTTTATGAAA 7812
OY      291 TGGTAGACAATTCTTAAGATATGGAAGATCGTTTATTAAGAAATAACCTGACTTTTGA 350

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Db      7813 TATTAAGTAAGTATTATAGTATATTTGAAATGTTATGTAATTTAGATTTTGTGTTTA 7872
Qy      351 AGTCATATATCTCAAAAACATTTGGAATGTCCTGAGCTTGAAATAACATGAGTGC 410
Db      7873 GAGAACTTTGGAATATATGTTTTTTTATTAATGTTAGTTTTTAATGGAAGTTGG 7932
Qy      411 TTATTCAGATGACGATTAATTTATTTAGCATAATTTTTCTCTGACAGAAATTCACCT 470
Db      7933 TTTTATGAAAGTAATTAATTAATGATTAATGATTAATGATGATGATTAATGAGTTTAA 7992
Qy      471 GGAGGAAATGCAACATCAATCCGCAAGATTTTAAATTAATGATTTCTATTTAC 530
Db      7993 ATAGTATTTT---AATTGAAATATGAAATTTGTTAAATTAAGATATATATTTGT 8048
Qy      531 CTATCTGCTGTAACTTCACTGGGAGAGAGATTTTTCAAAACCTTTTACATGAT 590
Db      8049 TAAAAATGTTTTTGCTGATGATTTTAAATGATTTTGTGAGTTTAAATGGAATGTAT 8108
Qy      591 AGAGGCTAAATCATTTAGAAATTTATTT 618
Db      8109 AATTGTATATATTAATTAAGTATATATTT 8136
```

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RESULT 7
US-10-517-441-715
; Sequence 715, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOKENS, John
; APPLICANT: HARBEC, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 715
; LENGTH: 12610
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-715
```

```
Query Match      4.0%; Score 40.4; DB 7; Length 12610;
Best Local Similarity 45.9%; Pred. No. 3.2; Mismatches 206; Indels 4; Gaps 1;
Matches 178; Conservative 0; Mismatches 206; Indels 4; Gaps 1;

Qy      231 TGTCTGAGAAATTTATCAAGATATATGCTATCTTTCATCTGCACTATAGTAAAA 290
Db      7753 TGTGTGAGATTTGATGATGATATATATGTTATTTAAGAAATGTTTTTTTAA 7812
Qy      291 TGGTATCAAAATTTCTAAAGATATGCAAAATGTTTTTATTAAGATGAACCTGATTTGA 350
Db      7813 TATAAGTAAATTTATATGATATATTAAGAAATGTTATTTGTAATTTGTTT 7872
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Qy      351 AGTCATATATCTCAAAAACATTTGGAATGTCCTGAGCTTGAAATAACATGAGTGC 410
Db      7873 GAGAACTTTGGAATATATGTTTTTTTATTAATGTTAGTTTTTAATGGAAGTTGG 7932
Qy      411 TTATTCAGATGACGATTAATTTATTTAGCATAATTTTCTCTGACAGAAATTCACCT 470
Db      7933 TTTTATGAAAGTAATTAATTAATGATTAATGATTAATGATGATGATTAATGAGTTTAA 7992
Qy      471 GGAGGAAATGCAACATCAATCCGCAAGATTTTAAATTAATGATTTCTATTTAC 530
Db      7993 ATAGTATTTT---AATTGAAATATGAAATTTGTTAAATTAAGATATATATTTGT 8048
Qy      531 CTATCTGCTGTAACTTCACTGGGAGAGAGATTTTTCAAAACCTTTTACATGAT 590
Db      8049 TAAAAATGTTTTTGCTGATGATTTTAAATGATTTTGTGAGTTTAAATGGAATGTAT 8108
Qy      591 AGAGGCTAAATCATTTAGAAATTTATTT 618
Db      8109 AATTGTATATATTAATTAAGTATATATTT 8136
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RESULT 8
US-10-932-182A-166164/c
; Sequence 166164, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 166164
; LENGTH: 820
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-166164
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Query Match      4.0%; Score 40.2; DB 6; Length 820;
Best Local Similarity 41.8%; Pred. No. 2.2; Mismatches 338; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

Qy      70 ATAGTACGTATATCTAACTTAAAGCAACAGATGAGGTCATACATCATATGGAAT 129
Db      594 ATATATATCTTATACATATCATTTACAAATATGTCATTTTATATATCTTTACC 535
Qy      130 GAATATCGAGCTAAAGAAATATATTTAGCTTACGCTTGGCTGATGCTATTTATAT 189
Db      534 CTATTAATATATATAAATAATTTCTATTAATATATATTTCTTAATCCAGATTTAT 475
Qy      190 GTATCTAAACTTCGATGACATATTAAGAAATAAGACGCTGAGGAATTTATCA 249
Db      474 ATATATATATATATATATATATTTTATTAATTAAGATTAATTTATTAATTAATA 415
Qy      250 GAATATATGCTAAATCTTTCATCTGACATATAGTGAATAATGTCATCAATTTCTAA 309
Db      414 ATTTATAGGCTTACTTCTGTTTAACTAATTAATGTAATATTTAACTTACTGCTCAAC 355
Qy      310 GATATGCAATATGTTTTTATTAAGATGACATGATTTGAAAGTCATATCTCAAAAC 369
Db      354 TATATTAATTAATGATTAATGATTTATGCTAATTTCCAAACATTAACATCAATCA 295
Qy      370 ATTTGAATGTCCTGAGCTGAAATAACATTAACATGAGGCTATTCAGATGAGATAA 429
Db      294 TATATATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 235
Qy      430 TTATAGCACTATATTTTCTCTGACAGAAATTTCACTGGAGAAATCAACATCA 489
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	Query Match	4.0%;	Score 40;	DB 6;	Length 1691140;
	Best Local Similarity	42.9%;	Pred. No. 9.1;		
	Matches 199;	Conservative	0;	Mismatches 265;	Indels 0; Gaps 0;
QY	143	AGAAATATATATTAGCTTACGCTTGGCTGTAGTGTATTCATATATGATCTAACTTC	202		
Db	543957	ATATAAAATATATATAGTTTAAAGACTATATATCTAGCGAGTTCTTTTGTTCTTAAAGCTC	544016		
QY	203	CTGATGACATATATTAAGATAAAGACCTGCTGAGGAATTTATCAAGAATATATATGCTA	262		
Db	544017	CCTGACACTTGGTGAACCAATATAGTTTATTAAGCAATAGTTTGTTATTTGATTTTATATC	544076		
QY	263	ATCTTTCAATCTGCACATATTAGTGAAATGTGTATCAAAATTTCTAAAGATATGCAATG	322		
Db	544077	AGAAAGCTTAATATGATATTTTAAATAAAGCTTCATATATATCAATCTTATTTGGAAAAA	544136		
QY	323	GTTTTATTAAGATGAATGATGATTTTGAAGTCAATATCTCAAAACATTGGAAATGTC	382		
Db	544137	GTAATTTGAAAAGCTCACTCAAGCTTCCCCGTGTGTTTATCTAGAAATATTAAAGCTTT	544156		
QY	383	CTGAGCTTGAAAAATAAACCATTGAGTCTTATTCAGATACGATTAATATTATAGCACTAT	442		

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Query March 3.9%; Score 39.8; DB 8; Length 37627;
Best Local Similarity 47.7%; Pred. No. 5.3;
Matches 116; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY      67  GATATAGTACGTAACTTAAAGCAAGATGAGGGTCATACAGCATCATATGGA 126
      |||||
Db      14013 GTATATAAAGAGTGCATATAAATACTAGTATATTTATGATATACAAAGTTGTTAACAA 140722
QY      127  ATTGAATATGAGCTAAGAAAATTAATTTAGCTTACGCTTTGGCTGTAAAGTGTATTCA 186
      |||||
Db      14073 AGATGGATGAGGTATTAAGTATTAATTTAGTTAATACGCCACAAAATGTGGCTTAAGT 141322
QY      187  AATGTATCTAACTTCCTGATGACATCTTATTAAGAAATTAAGAGACTGCGAGAAATTTAT 246
      |||||
Db      14133 GGTCAATTGACAAATTAAGAGATATTAACAAAATTAAGAGACAAAGGCTTAATTTATA 141922
QY      247  CAAGAAATATATGTCTATATCTTTCATCTGACATTAATAGTGAATAATGSGATCAAAATTTCT 306
      |||||
Db      14193 CTGGAAATTCCTTGTATCAATTTGGCTAAACAAAACCAAGTACGTATGACCAAAATAGCT 142522
QY      307  AAA 309
      |||
Db      14253 AAA 14255

RESULT 11
US-10-932-182A-76518
; Sequence 76518, Application US/10932182A
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

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/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 76518
/ LENGTH: 2460
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-76518

Query Match
Best Local Similarity 51.1%; Pred. No. 3.7;
Matches 93; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 134 ATCGAGCTAAGAAAATAATTTAGCTTACCGCTTGGCTGTAAGTGTATTCATTAAGTAT 193
DB 1475 ATATTAATATATATATATCTTACTTCCAAATACATTAGAAATTAATTAATTAATGATA 1534
QY 194 CTAACTCTGATGACTATTTATTAAGATTAAGAGACTGCTGAGAAATTTATCAAGAA 253
DB 1535 GTHATACAGTATGACAAACCAAAAACAAAAAATATTAATAAAAGTTTCATGATA 1594
QY 254 ATATGCTATATCTTTTCATCTGACATTAAGTGAAATGCTGATCAAAATTTCTTAAGATA 313
DB 1595 ATGAATGTATCTACTTTTGTATACATCTGATGAAATATATGATGATGATGATGATA 1654
QY 314 TG 315
DB 1655 TG 1656

RESULT 12
US-10-517-441-414/C
/ Sequence 414, Application US/10517441
/ GENERAL INFORMATION:
/ APPLICANT: FOEKENS, John
/ APPLICANT: HARBECCK, Nadia
/ APPLICANT: KOENIG, Thomas
/ APPLICANT: MAIER, Sabine
/ APPLICANT: MARTENS, John
/ APPLICANT: MODEL, Fabian
/ APPLICANT: NIMMIRICH, Inko
/ APPLICANT: RUJAN, Tamas
/ APPLICANT: SCHMITT, Armin
/ APPLICANT: SCHMITT, Manfred
/ APPLICANT: LOOK, Maxime P.
/ APPLICANT: MARX, Almuth
/ APPLICANT: HOEFLEER, Heinz
/ TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
/ TITLE OF INVENTION: proliferative disorders
/ FILE REFERENCE: 47675-93
/ CURRENT APPLICATION NUMBER: US/10/517,441
/ CURRENT FILING DATE: 2004-12-11
/ PRIOR APPLICATION NUMBER: PCT/EP2003/010881
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: DE 10317955.0
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: DE 10300096.8
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: DE 10245779.4
/ PRIOR FILING DATE: 2002-10-01
/ NUMBER OF SEQ ID NOS: 2147
/ SEQ ID NO 414
/ LENGTH: 19634
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-414

Query Match 3.9%; Score 39.2; DB 7; Length 19634;
```

```
Best Local Similarity 44.7%; Pred. No. 6.5;
Matches 152; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 245 ATCAAGATATATATGCTATCTTTTCATCTGACATTTAGTGAAATGATGATCAAAATTT 304
DB 10985 ATTAATCTTTAATATATATTTATATATATCCATACAAATTAATAATTTAATCAATATA 10926
QY 305 CTAAAGATATGCAAAATGTTTTTATTAAGAAATGAATCGAATTTTGAAGTCAATATCTCTC 364
DB 10925 CTCTAACAAAAAATAATTTCTTAATAATACCTTTATTTATTAACCTCAATTTCTAAA 10866
QY 365 AAAACATTTGAATTTCTGAGCTTGAATAATTAACATGAGTCTTATTCAGATGACG 424
DB 10865 TAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10806
QY 425 ATAAATTTATGACATATATTTTTCTGTCGACGAATTTCCACTGAGAGAAATCAAC 484
DB 10805 TTCAATATTAATTAATTAATTAATTTCTTTTCATTAATATCAATATTAATAATATACCTTT 10746
QY 485 ATCAAAATGCCCAAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 544
DB 10745 TCTAAACTATATCAATTAATAATTAATAATTAATAATTAATTAATTAATTAATTAATTA 10686
QY 545 CTTCACGTGGAGAGAGATTTTTCAAAAAATTTTACAA 584
DB 10685 ATATATATCAATCAATCAATTTTAAATAATTAATTAATAAA 10646

RESULT 13
US-10-517-441-688/C
/ Sequence 688, Application US/10517441
/ GENERAL INFORMATION:
/ APPLICANT: FOEKENS, John
/ APPLICANT: HARBECCK, Nadia
/ APPLICANT: KOENIG, Thomas
/ APPLICANT: MAIER, Sabine
/ APPLICANT: MARTENS, John
/ APPLICANT: MODEL, Fabian
/ APPLICANT: NIMMIRICH, Inko
/ APPLICANT: RUJAN, Tamas
/ APPLICANT: SCHMITT, Armin
/ APPLICANT: SCHMITT, Manfred
/ APPLICANT: LOOK, Maxime P.
/ APPLICANT: MARX, Almuth
/ APPLICANT: HOEFLEER, Heinz
/ TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
/ TITLE OF INVENTION: proliferative disorders
/ FILE REFERENCE: 47675-93
/ CURRENT APPLICATION NUMBER: US/10/517,441
/ CURRENT FILING DATE: 2004-12-11
/ PRIOR APPLICATION NUMBER: PCT/EP2003/010881
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: DE 10317955.0
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: DE 10300096.8
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: DE 10245779.4
/ PRIOR FILING DATE: 2002-10-01
/ NUMBER OF SEQ ID NOS: 2147
/ SEQ ID NO 688
/ LENGTH: 19634
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-688

Query Match 3.9%; Score 39.2; DB 7; Length 19634;
Best Local Similarity 44.7%; Pred. No. 6.5;
Matches 152; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 245 ATCAAGATATATATGCTATCTTTTCATCTGACATTTAGTGAAATGATGATCAAAATTT 304
DB 10985 ATTAATCTTTAATATATATTTATATATATCCATACAAATTAATAATTTAATCAATATA 10926
QY 305 CTAAAGATATGCAAAATGTTTTTATTAAGAAATGAATCGAATTTTGAAGTCAATATCTCTC 364
DB 10925 CTCTAACAAAAAATAATTTCTTAATAATACCTTTATTTATTAACCTCAATTTCTAAA 10866
QY 365 AAAACATTTGAATTTCTGAGCTTGAATAATTAACATGAGTCTTATTCAGATGACG 424
DB 10865 TAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10806
QY 425 ATAAATTTATGACATATATTTTTCTGTCGACGAATTTCCACTGAGAGAAATCAAC 484
DB 10805 TTCAATATTAATTAATTAATTAATTTCTTTTCATTAATATCAATATTAATAATATACCTTT 10746
QY 485 ATCAAAATGCCCAAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 544
DB 10745 TCTAAACTATATCAATTAATAATTAATAATTAATAATTAATTAATTAATTAATTAATTA 10686
QY 545 CTTCACGTGGAGAGAGATTTTTCAAAAAATTTTACAA 584
DB 10685 ATATATATCAATCAATCAATTTTAAATAATTAATTAATAAA 10646
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